Remarks

Claims 63, 84 and 104 have been amended. Support for the amendments lies in the original claims and specification as filed, and no new matter is added by virtue of these amendments. Entry and consideration of the amendment and remarks provided herein is respectfully requested. The Final Office Action included claim rejections under 35 USC §§112, 102 and 103; each of these rejections is addressed individually below.

Specification Objections

The specification was objected to as failing to provide proper antecedent basis for the claimed subject matter. The Examiner indicated the specification does not appear to provide antecedent basis for the language "specific predefined proteins" as recited in claims 63 and 84.

Applicants have previously argued that the specification does indeed provide support for this language by pointing out that, for example, original claim 27 included the phrase "specific predefined ligand", and that a protein in the context of present claims 63 and 84 is merely one type of ligand.

The Examiner has acknowledged that the specification fully supports the phrase "specific predefined ligand" (see page 15 of the Final Office Action). However, the Examiner has requested that Applicant point out where in the specification there is support for the "alleged subset relationship between protein and ligand" (see footnote 5 on page 15 of the Office Action).

Applicants respectfully direct the Examiner's attention to paragraph [0029] of the specification, which begins "While this patent application generally refers to removal of proteins from a sample, the same techniques may be used for removing any ligand . . . ". The specification therefore clearly indicates that specific predefined proteins are examples of specific predefined ligands.

Indeed, much of the specification is directed to discussions of removal of specific predefined proteins. To give but a few examples:

(1) The Abstract refers to "Removal of abundant *proteins* from a sample . . . " and specifically refers to removal that is "accomplished by immunosubtraction . . .". Immunosubtraction is removal by binding to an antibody. Antibodies generally are highly specific. Thus, removal by immunosubtraction is, by definition, removal of "specific" (only those that bind to the antibodies) predefined (must have been if antibodies were obtained) proteins.

(2) The Summary begins "It is an [sic, a] purpose of the invention to provide a method and means for selectively removing desired, undesired and/or abundant *proteins* . . . ".).

(3) Paragraph [0028] of the Detailed Description states "The *proteins* to be removed from the sample are done so by exposing the sample to *receptors* that *specifically* bind the proteins to be removed." This paragraph alone provides explicit support for removal of "specific predefined protein". The Examiner's objection should be removed.

Applicants also note that, in commenting on the sufficiency of the specification with respect to the phrase "specific predefined ligand", the Examiner "posits" that persons skilled in the art recognize that the objects and/or steps required for "predefining" proteins is not necessarily or inherently the same as the objects and/or steps required for predefining "ligands" (see page 15 of the Office Action).

Applicants are puzzled by this comment. Those of ordinary skill in the art, reading the present specification, understand the objects and/or steps required for predefining ligands, and further understand that some ligands are proteins. When the ligand is a protein, as is the case in claims 63 and 84, then the objects and/or steps required for predefining the ligand are indeed necessarily and inherently the same as the objects and/or steps required for predefining the protein.

Moreover, the clear focus of the present specification is on the removal of proteins, and in particular on the removal of specific predetermined proteins (i.e., those that interact with a particular receptor such as an antibody). There is extensive discussion of *why* it is desirable to remove proteins, and *which* proteins might be useful to remove (e.g., abundant proteins, or otherwise contaminating proteins that can complicate interpretation of a complex sample (see, for example, Background and Summary; see also paragraphs [0021] – [0026]; see also paragraph [0087]; see also paragraphs [0092] – [0096], etc.), as well as great detail on how to accomplish the removal (see Detailed Description generally and Exemplification in particular). Thus, there can be no question that the present specification fully describes the objects and/or steps required for predefining proteins.

Rejections under 35 U.S.C. § 112

Claims 32, 52, 62-69, 84-85, 88-89 and 104-107 were rejected under 35 USC §112, second paragraph as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

The Examiner objected to the recitation of "specific predefined proteins" in claims 63 and 84 as indefinite and lacking antecedent support in the specification. Applicants respectfully traverse the rejection.

For all of the reasons set forth above, Applicants respectfully submit that the phrase "specific predefined proteins" is fully supported by the specification and is understood by those of ordinary skill in the art. Solely for purposes of progressing the prosecution of this case, Applicants have amended the claim to revert to the "specific predefined ligands" language used in claim 27 as originally filed, and to then clarify that the "specific predefined ligands" are proteins. Applicants respectfully request that the rejection be removed.

The Examiner objected to the recitation of "solid phase matrices" in claim 63 as lacking antecedent basis and as indefinite. The rejection is traversed.

Applicants respectfully submit that there is no indefiniteness in the claim language as utilized, and that it is fully consistent with the specification. The present claims recited solid phase matrices comprising "a plurality of particles". The Examiner takes the position that there is some confusion because the specification at paragraph [0036] refers to "a matrix" as "a bead".

Applicants acknowledge (as they have previously done) the reference in paragraph [0036] to "a matrix" as "a bead". However, this is not the only reference to "a matrix" in the specification. As is typical in the art of chromatography, the term "matrix" is used in the specification to refer to the solid phase material with which a liquid is contacted. In principle, this can be a single bead (hence the single bead reference). More commonly, however, it is a collection of beads. Consistent with this, the specification also includes comments like "whether the matrix *is loose beads* . . . .", which is found at paragraph [0050].

Those of ordinary skill in the art, reading the specification, understand that a single bead can be considered "a matrix", and that a matrix can be comprised of multiple beads. Thus, the specification contemplates embodiments in which a matrix is formed of a *single* particle (e.g., bead) and those in which a matrix is formed of a *plurality* of particles (e.g., beads). The present claims are directed only to those embodiments in which a matrix is comprised of a *plurality* of particles. The language of the claims is definite with regard to the plurality.

The Examiner has also taken the position that there is some indefiniteness around the concept of a "mixture", stating that it is unclear "how a matrix of beads that is stacked, layered and/or adjoined on/to another matrix of beads can be 'present as a mixture'". Applicants respectfully submit that, given that the claims clearly recite at least two distinct solid phases, each

of which comprises a plurality of particles, the recitation of "a mixture" is perfectly clear. For example, when the particles are beads so that the first solid phase is a first set of beads, and the second solid phase is a second set of beads, the claims are satisfied when the two sets of beads are present as a mixture. A layer of one set of beads sitting on top of a layer of another set of beads is not a mixture; it is two stacked layers. Indeed, the specification explicitly addresses two *different* embodiments of the invention with regard to use of different matrices carrying different binding agents, stating that they can be "mixed before adding" *or* "loaded sequentially" (see paragraph [0066]. The "mixed before adding" embodiment, of course, generates a mixture as recited in the present claims. The "loaded sequentially" embodiment creates layers. These are two *different* embodiments that are set forth in the specification. The present claims clearly recite only one. Those of ordinary skill in the art understand what is meant by a "mixture". The present claims are definite and the rejection should be removed.

Rejections under 35 U.S.C. § 102(b)

Claims 32, 52, 62-69, 84, 89 and 104 were rejected under 35 USC § 102(b) as being anticipated by Stausbøl-Grøn, et al., 391 *FEBS Letters* 71 (1996). This is not a new rejection, but frankly is one that is quite troubling to Applicants. The differences between Stausbøl-Grøn and the claimed invention are numerous, and with each exchange the Examiner maintains the rejection based on comments that are more and more troubling. The Final Office Action includes both a repetition of the prior rejection and responses to Applicant's prior arguments. Applicant will attempt to address both herein.

To begin, Applicant notes that Stausbøl-Grøn describes "a phage display subtraction method with potential for analysis of differential gene expression" (see Title). The method is illustrated in Figure 1 of the reference. In brief, the idea is to identify phage that bind to proteins that are differentially expressed between two sources. This is accomplished by affixing proteins from one source to the surface of a tube. Proteins from the second source are affixed to beads. A sample of phage displaying different antibodies on their surfaces is then introduced into the tube. More of the first source proteins can also be added if desired. Phage that bind to proteins *common* between the two sources will stick to the sides of the tube or complex with the first source proteins in solution and therefore will not be available to bind to the second source proteins on the beads. Phage that bind *only* to proteins in the second source, however, will bind to the beads. The beads are then isolated and second-source-specific phage are identified.

A comparison of this method to the claims reveals many differences. Independent claims 63 and 84 each recite methods that involve "removing at least two specific predefined ligands from a sample . . . thereby producing a modified sample", and then "recovering the modified sample". In each case the "removing" step involves contacting the sample with an affinity binding composition that comprises a mixture of particles carrying receptors that bind to the specific predefined ligands, thereby removing them from the sample so that the modified sample is produced.

As an initial matter, it is not clear what the Examiner considers to be the "sample" when levying the anticipation rejections, and what the Examiner considers to be "removed" from the sample. With reference to "removing", the Examiner points to page 72, column 1, fifth paragraph of Stausbøl-Grøn, where it is said that the "immunobead was washed". The "immunobead" referred to at that point is the bead containing second source proteins *after* it is isolated. Thus, it is difficult to understand how "washing" this immunobead could constitute "removing" specific predefined proteins from a sample as recited in the present claims. The present claims require removal by binding. Washing removes things that are not bound. The present claims require removal from a sample that is contacted with an affinity composition. Washing the immunobead removes *from* an affinity composition and not from a sample. Thus, the portion of Stausbøl-Grøn pointed to by the Examiner as teaching "removing" does not teach any action related to the "removing" step recited in the present claim.

However, the Examiner's own rejection is not consistent in its references. In the same sentence that makes the above-discussed reference with regard to "removing", the Examiner indicates that the relevant "at least two specific predefined proteins" are the "Competitive proteins" referenced on page 72, column 2, second paragraph. The competitive proteins referred to at this location are the additional source one proteins added to the solution when the phage sample is introduced into the tube (coated with source one proteins) with the beads (coated with source two proteins). These proteins are not removed in the Stausbøl-Grøn system. Indeed, these proteins are affirmatively *added* to the sample! Furthermore, these proteins are not "removed" when the "immunobead was washed". Thus, the Examiner's reference for "removing" and the Examiner's citation for "at least two specific predefined proteins" are internally inconsistent.

In a further inconsistency, when referring to "producing and/or recovering the modified sample", the Examiner points to a statement in the Abstract relating to "enrich(ing) selectively phage displayed antibodies directed against proteins constituting a difference between two populations of cells". If the modified sample is the phage sample that is enriched for antibodies

directed against different proteins (i.e., for antibodies that bind to the second source proteins [on the beads] and not to the first source proteins [on the tube and in solution], then presumably the "sample" was the original phage sample. In this portion of the rejection, the Examiner points to the "immunobeads" as "a first and second solid phase matrix", and to two different kinds of proteins that are present on the immunobeads (i.e., LDH and the MIX proteins) as the first and second receptors.

Even this interpretation of Stausbøl-Grøn cannot anticipate the claims. As Applicants have previously pointed out, what is removed from the "sample" under this interpretation of Stausbøl-Grøn are phage – specifically, phage that bind to the first source proteins on the tube and in solution. Applicants have previously pointed out that one of ordinary skill in the art would not consider removal of phage to be removal of "specific, predefined proteins". The Examiner has rejected this point by referring to particular proteins that are produced by the phage and noting that these proteins are in fact removed as "attached to a phage" (see page 17 of the Final Office Action). Indeed, the Examiner points to two different kinds of proteins as being removed – "single chain Fv antibody fragments" discussed on page 71 of Stausbøl-Grøn, and "coat protein" discussed in the Introduction.

The Examiner's choice of proteins that are said to be removed from the same makes clear one of several failures in the rejection. The "coat protein" the Examiner refers to is the minor coat protein of the phage, with which displayed proteins are typically fused. Of course, coat protein is not specifically depleted from the sample in Stausbøl-Grøn. Coat protein is part of the phage. It is present in the removed phage, but it is also present (presumably at the same relative amount) in the phage that remain in the enriched sample.

Regardless of whether phage can be considered to be "proteins" and regardless of whether particular phage-associated proteins are or are not specifically depleted in Stausbøl-Grøn, the reference cannot anticipate the present claims. There is no reading of Stausbøl-Grøn that can teach or suggest a mixture of matrix particles having different binding specificities as is recited in the present claims. Applicant made this point in a previous Response and the Examiner has now offered three different interpretations of "first and second solid phage matrix" (see pages 18 and 19 of the Final Office Action). Applicants address each of these in turn below.

In the first interpretation, the Examiner appears to assert that the immunobeads coated with second source proteins are *both* solid phases. The Examiner specifically points to paragraph 72, column 1, sixth paragraph, where reference to addition of "five immunobeads" to an immunotube is

made. These immunobeads cannot anticipate the first and second solid phase matrices recited in the present claims for at least three reasons: (1) they are all identical (the complete description is "five immunobeads coates with FM55p proteins were added); thus by definition there is no set of at least two beads (as would be minimally required for each solid phase matrix recited in the claims since each is said to comprise "a plurality" of particles) that have the same binding specificity as each other but different from another set of at least two; (2) the beads are not contacting one another (they are five beads floating in a tube – even as depicted in Figure 1, to which the Examiner makes reference, they are five isolated beads); and (3) they are not present as a mixture (as indeed they cannot be if they are not different, and cannot be if they are not in contact with one another). The Examiner actually does not even suggest that the beads are present as a mixture. Tellingly, the Examiner's comments actually state that the beads are "in a mixture", as if the fact that they are added to a solution containing other components were relevant. The claims recite that particles of different solid phase matrices are present "as a mixture", meaning that they are not in layers but rather are mixed together with one another.

In the second interpretation, the Examiner states that Stausbøl-Grøn teach a plurality of solid phase matrices because it mentions a "naïve phagemid library" at page 71, fight column, last paragraph, second sentence. This interpretation is not understood at all, as there is no suggestion anywhere that such a library involves a solid phase, let alone two different particulate solid phase matrices having different binding specificities and present as a mixture. Indeed, a close read of the reference shows that this library, which is described in Section 2.1 at the top of the left column on page 72, is "a naïve phagemid library of approximately 10^8 *clones* of scFv expressed on phage". It seems rather unlikely that these clones were associated with any solid phase, as they were apparently introduced into two different bacterial strains "to produce phage displayed scFv and soluble scFv". Even if the clones were at some point associated with a solid phase, there is no indication that it might have been a particulate solid phase, let alone two different particulate solid phases. Moreover, there is no indication that this library was ever contacted with a sample from which it depleted anything by binding to it. Reference to the phagemid library in Stausbøl-Grøn is not relevant to the present claims.

In the third interpretation, the Examiner simply states that Stausbøl-Grøn teach a first and second solid phase matrix wherein the solid phase matrix is a bead. Applicants do not dispute that Stausbøl-Grøn teach a bead. For all of the reasons discussed above, a bead is not a solid phase matrix comprising a plurality of particles. Moreover, a bead is not *two different* solid phase

matrices having different binding specificities. Least of all a bead is not a *mixture* of *two different* solid phase matrices (each comprising a *plurality of particles*) having *different binding specificities.*

Thus, none of the interpretations of Stausbøl-Grøn put forth by the Examiner, either in the original rejection or in the Final Office Action, can anticipate the present claims.

Rejections under 35 U.S.C. § 102(e)

Claims 32, 52, 62-69, 84, 88-89, 104, and 110-113 stand rejected under 35 USC § 102(e) as being anticipated by Payan (US Patent 6,455,263). This rejection is emphatically traversed.

Payan describes a system for identifying binding partners of a known target. In this system, candidate binding partners are covalently attached to beads. The beads are then contacted with a known target that is either directly labeled with a fluorescent label, or can be indirectly so labeled so that the target binds to any partners present in the collection of beads. The beads are then sorted by FACS.

By contrast, the present claims recite a method in which a sample that contains at least two predetermined proteins to be removed and a plurality of proteins that will remain is contacted with at least two solid phase matrices having different binding specificities, where each of the solid phase matrices comprises a plurality of particles and are in contact with one another as mixture, so that the specific predetermined proteins bind to receptors on the different solid phases and are thereby depleted from the sample, producing a modified sample (containing a plurality of proteins) that is collected.

Once again, the Examiner's rejection is confusing. The Examiner asserts that Payan describes a method for separating proteins. When referring to "separating", the Examiner points to column 13, lines 1-2, which discusses sorting beads by FACS. When referring to the "proteins", the Examiner points to the "library of candidate agents" at column 3, lines 48-49, to the "third, fourth, etc. populations of target molecules" at column 14, lines 24-25, and to the "candidate bioactive agents", which can be proteins, at column 3, lines 28-30. This is confusing because the Examiner is referring to two different things as the "protein" that is "separated" – the "candidate agents", which are the candidate binding partners bound to the beads, and the "populations of target molecules", which are the target molecules for which a binding partner is sought. It cannot be both.

Assuming, *arguendo.* That the Examiner is interpreting the beads bound to "candidate bioactive agents" to represent solid phase matrices (with attached receptors) as recited in the present claims, then whether the "candidate bioactive agents" are or are not proteins is irrelevant.

Similarly, the Examiner asserts that Payan teaches "recovering a modified sample" because Payan refers to "collecting" at column 2, lines 64-65 and to "sorting results in a population of non-fluorescent beads" in column 13, lines 10-11. This makes no sense. According to the present claims, what is "recovered" is a "modified" sample – that is, a sample that contains a plurality of proteins and has been depleted of at least two proteins by virtue of having been contacted with at least two particulate solid phase matrices, present as a mixture and having different binding specificities. By contrast, what is "collected" at column 2, lines 64-65 is beads that *used* to be bound to target but aren't anymore. That is, Payan teaches that, after target binds to candidate bioactive agent on a solid phase, the target is labeled and the beads are sorted. Target can then be released from the beads, and the newly non-flourescent beads are "collected" at column 2, lines 64-65. This is irrelevant to the present claims.

Column 13, lines 10-11 refers more generally to the FACS sorting of the original target sample + solid-phase-bound candidate agents combination. Importantly, this sorting generates two populations: one of beads bound to labeled target, and one of beads not bound to labeled target. There is no modified target sample containing a plurality of proteins but depleted of those that bound to the beads.

Indeed, in almost every embodiment presented in the Payan patent, beads are contacted with a sample that contains only one target. Of course, even when the beads are contacted with two or more target molecules at a time, the intention is that *each and every* target molecule be bound by at least one bead-bound candidate agent. Thus, the target sample described by Payan does not include a plurality of proteins that are not bound by solid-phase-associated receptors as recited in the present claims. Thus, no "modified sample" is ever produced. Furtermore, even if there were a case under Payan where no binding partner were found for a particular target so that arguably removal of the other (bound) targets from that target could constitute production of a "modified sample" according to the present claims, there is no recovery of that modified sample. Indeed, Payan teaches strongly away from any such recovery by focusing entirely on FACS sorting. FACS sorting, as taught by Payan, will collect *beads* in two populations: fluorescent and non-fluorescent. What happens to unbound components of the original target sample during that process is completely unclear, but certainly no specifically depleted modified version of it could every be collected under the teachings of Payan. Indeed, once the beads are sorted, they are washed. All unbound proteins are discarded.

Thus, Payan does not teach (1) a sample comprising at least two specific predefined proteins to be depleted and a plurality of other proteins; (2) production of a modified sample depleted of the at least two specific predefined proteins but containing the other plurality of proteins; or (3) recovery of a modified sample. Indeed, Payan teaches strongly away from production and recovery of a modified sample.

Furthermore, although Payan teaches beads bound to candidate binding agents, Payan does not teach at least two solid phase matrices comprising a plurality of particles and differing in binding specificity. Furthermore, Payan is very general about the composition of agent-bound beads (discussed, for example, at column 9, line 60 – column 10, line 21). There certainly is no specific teaching or suggestion of the particular arrangement recited in the claims. Moreover, Payan *requires* that each bead be separately sorted. This is the essence of FACS sorting. Thus, Payan *cannot* teach or suggest, and indeed teaches strongly away from, at least two solid phase matrices comprising a plurality of particles *in contact with* one another and *present as a mixture.*

For at least all of these reasons, Payan cannot anticipate the present claims. Indeed, Payan's methods teach strongly away from the presently claimed methods. The rejection should be removed.

Rejections under 35 U.S.C. § 103(a)

Claims 32, 52, 62-69, 84-85, 88-89 and 104-107 were rejected under 35 USC § 103(a) as being unpatentable over Davies (U.S. Patent 6,696,304) in view of Payan (U.S. Patent 6,455,263). This rejection is also strongly traversed.

As Applicants have previously discussed, Davies provides a system for quantifying the amount of protein (or other amine-containing analyte) in a sample. This quantification is performed by (1) immobilizing on a solid phase (by adsorption or covalent conjugation) protein present in a sample containing an unknown amount of the protein; (2) covalently binding a light-emitting signal molecule or label to the bound protein; and (3) comparing the intensity of the light emitted from the label to that emitted from standard microparticle preparations with a known amount of reference material (see, for example, Summary of the Invention, Column 3, line 60 – Column 4, line 9). Thus, the teaching of Davies are limited to quantifying the amount of a protein that is irreversibly bound to a solid phase particle. Indeed, Davies calls this out as a key feature of his invention. Specifically, column 17, lines 27-38 reads:

> "The invention differs from existing methodologies in that the all components in this assay are bound in a sequential manner *covalently or irreversibly* at the microparticle surface. This feature is distinct from any prior art approaches to protein quantitation, which inveaiably (sic, invariably) involves non-covalent associations, viz., as in the Lowry protein method, Bradford dye binding protein assay, amido Black method, or colloidal gold method. This novel approach permits not only the enhancement of the detection threshold by several orders of magnitude, but also an efficient separation of bound and unbound reagents through a series of wash steps and thus reducing the background noise."

Davies does not teach or suggest a sample containing at least two proteins to be depleted and a plurality of other proteins to remains as a modified sample. The proteins discussed by Davies are those that are to be quantitated. They are quantitated by being permanently associated with a particulate solid phase. Anything not attached to the solid phase is discarded.

Davies does not teach at least two solid phase matrices comprising particles and having different binding specificities that are in contact with one another and present as a mixture. Davies does teach a solid phase comprising a plurality of particles. Davies also teaches that different particulate solid phases can be prepared, and can be combined with one another (see column 9, lines 38 – 53). In such an embodiment, individual solid phases that have different size or fluorescent attributes and known amounts of reference markers can be prepared and combined as standards. A particular test solid phase with an unknown amount of protein attached (and yet different size or fluorescent attributes) can further be added to the combination. However, there is no requirement that the solid phases be in contact with one another; nor is there any requirement that the particles be present as a mixture (though they may be). Moreover, no combined solid phase is ever contacted with a sample from which proteins are to be depleted. All that is ever done with such a solid phase is that it is subjected to analysis of the different light-emitting properties of the solid phases, so that the amount of protein on the test solid phase is determined.

It should be noted that, in the original rejection, the Examiner asserted that combination of a test solid phase with a set of solid phase standards constitutes "contacting a sample with an affinity binding composition". This is simply incorrect. There is no "binding" between the solid phase

standards and the test solid phase. They are simply present together so that the level of light they emit is internally controlled.

There is no combination of Davies with Payan that could possibly render obvious the presently claimed invention. It is not even clear how or why one of ordinary skill in the art would combine Davies and Payan. As discussed, Payan teaches a system for identifying a binding partner for a known target by immobilizing candidate targets on beads, biding them with fluorescent partner, and sorting by FACS. Davies teaches a system for quantifying a permanently immobilized amine-containing analyte on a particulate solid phase. If the Examiner is suggesting that a person of ordinary skill in the art would use the combined solid phases described by Davies in a binding assay as described by Payan, there would be no motivation to do so. All but one of the solid phases is Davies' combinations are reference solid phases – not expected to have any interesting binding characteristics for analysis according to Payan. There would be no need to include them in the Payan assay. Moroever, even if they were included, the result would be a binding assay, followed by FACS. As discussed above with reference to Payan, there would be no sample comprising at least two specific predefined proteins to be depleted and a plurality of other proteins; production of a modified sample depleted of the at least two specific predefined proteins but containing the other plurality of proteins; or recovery of a modified sample. Moreover, there would be no teaching or suggestion of the recited solid phases "in contact" and "present as a mixture". FACS sorting precludes this.

In summary, there is no motivation to combine the teachings of Davies and Payan, and even if such a motivation existed, the resulting combination still would not teach each of the features of the claimed invention. Applicants therefore submit that the instant claims are not obvious for each of the foregoing reasons. Withdrawal of the rejection is respectfully requested.

In conclusion, in view of the remarks presented herein, none of the cited art anticipates any of the claims pending in the instant application nor renders them obvious. Applicants therefore respectfully submit that the present case is in condition for allowance. Early Notice to that effect is respectfully requested.

If, at any time, it appears that a phone discussion would be helpful, the undersigned would greatly appreciate the opportunity to discuss such issues at the Examiner's convenience. The undersigned can be contacted at (617) 248-5000 or (617) 248-5175 (direct dial).

This response is being filed via facsimile on January 17, 2007. It is believed no additional fees are due in connection with this submission. However, in the event any additional fees or extensions are due, please consider this a petition therefore, and please charge any fees associated with this filing, or apply any credits, to Deposit Account No. 50-1078.

Respectfully submitted,

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